

## SEQUENCE LISTING

<110> Lok, Si  
Holloway, James L.

<120> Human V2 Vomeronasal Receptor

<130> 00-107

<150> 60/252.373

<151> 2000-11-21

<160> 10

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 657

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(657)

<400> 1

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1 5 10 15

ttt ctt gca ttt tta tgg gct gaa ttg ggc tct gaa gcc aaa gaa gag 96  
Phe Leu Ala Phe Leu Trp Ala Glu Leu Gly Ser Glu Ala Lys Glu Glu  
20 25 30

aaa gaa gaa gaa cgg acc tgc cgg ttg ctg ggc aag tgt gta gat gcc 144  
Lys Glu Glu Glu Arg Thr Cys Arg Leu Leu Gly Lys Cys Val Asp Ala  
35 40 45

gaa aac cat tcc ctt gtt att gga gga ctg ttt cct att gac tcc agg 192  
Glu Asn His Ser Leu Val Ile Gly Gly Leu Phe Pro Ile Asp Ser Arg  
50 55 60

acc atc cca gca aat gag tct att ttg gag cca gca tca gca aaa tgt 240  
 Thr Ile Pro Ala Asn Glu Ser Ile Leu Glu Pro Ala Ser Ala Lys Cys  
 65 70 75 80

gaa ggg ttt aac ttt cag aga ttc cgc tgg atg aaa gcc atg atc cac 288  
 Glu Gly Phe Asn Phe Gln Arg Phe Arg Trp Met Lys Ala Met Ile His  
 85 90 95

atg atc aag gag att aat aag agg aag gat att ttg ccc aac atc act 336  
 Met Ile Lys Glu Ile Asn Lys Arg Lys Asp Ile Leu Pro Asn Ile Thr  
 100 105 110

ctg ggc tat cag atc ttt gat acc tgt ttt acc atc tcc aaa tca gtg 384  
 Leu Gly Tyr Gln Ile Phe Asp Thr Cys Phe Thr Ile Ser Lys Ser Val  
 115 120 125

gaa gca gtc ttg gta ttt ctt aca ggg cag gaa gaa aac agg ccc aat 432  
 Glu Ala Val Leu Val Phe Leu Thr Gly Gln Glu Glu Asn Arg Pro Asn  
 130 135 140

ttt aga aac agc act gga gca ttt ccg gca gga att gtt gga gca ggt 480  
 Phe Arg Asn Ser Thr Gly Ala Phe Pro Ala Gly Ile Val Gly Ala Gly  
 145 150 155 160

gga tca ttc tta tca gtt cct gct tca aga att cta ggg tta tat tat 528  
 Gly Ser Phe Leu Ser Val Pro Ala Ser Arg Ile Leu Gly Leu Tyr Tyr  
 165 170 175

ttg cct cag gtg ggc tat acc tct acc tgc gtg att ctt agt gac aaa 576  
 Leu Pro Gln Val Gly Tyr Thr Ser Thr Cys Val Ile Leu Ser Asp Lys  
 180 185 190

tac cag ttt cca tct tat ctt cgt gta ata gcc agc gat aag atc cag 624  
 Tyr Gln Phe Pro Ser Tyr Leu Arg Val Ile Ala Ser Asp Lys Ile Gln  
 195 200 205

tcg aag gct gtg gta aaa cgt atc caa cac ttt 657  
 Ser Lys Ala Val Val Lys Arg Ile Gln His Phe  
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&lt;210&gt; 2

&lt;211&gt; 219

&lt;212&gt; PRT

<213> Homo sapiens

<400> 2

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Lys Glu Glu Glu Arg Thr Cys Arg Leu Leu Gly Lys Cys Val Asp Ala
      35           40           45
Glu Asn His Ser Leu Val Ile Gly Gly Leu Phe Pro Ile Asp Ser Arg
      50           55           60
Thr Ile Pro Ala Asn Glu Ser Ile Leu Glu Pro Ala*Ser Ala Lys Cys
65           70           75           80
Glu Gly Phe Asn Phe Gln Arg Phe Arg Trp Met Lys Ala Met Ile His
      85           90           95
Met Ile Lys Glu Ile Asn Lys Arg Lys Asp Ile Leu Pro Asn Ile Thr
      100          105          110
Leu Gly Tyr Gln Ile Phe Asp Thr Cys Phe Thr Ile Ser Lys Ser Val
      115          120          125
Glu Ala Val Leu Val Phe Leu Thr Gly Gln Glu Glu Asn Arg Pro Asn
      130          135          140
Phe Arg Asn Ser Thr Gly Ala Phe Pro Ala Gly Ile Val Gly Ala Gly
145          150          155          160
Gly Ser Phe Leu Ser Val Pro Ala Ser Arg Ile Leu Gly Leu Tyr Tyr
      165          170          175
Leu Pro Gln Val Gly Tyr Thr Ser Thr Cys Val Ile Leu Ser Asp Lys
      180          185          190
Tyr Gln Phe Pro Ser Tyr Leu Arg Val Ile Ala Ser Asp Lys Ile Gln
      195          200          205
Ser Lys Ala Val Val Lys Arg Ile Gln His Phe
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<210> 3

<211> 657

<212> DNA

<213> Artificial Sequence

<220>

<223> This degenerate nucleotide sequence encodes the amino acid sequence of SEQ ID NO:2.

<221> misc\_feature

<222> 12, 15, 33, 36, 39, 54, 57, 63, 69, 75, 78, 81, 87, 111.

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1 5 10 15

gga ttc gtt cag agg gaa cca ata tgc tgc ttt gac tcc atc cca tgt 96  
 Gly Phe Val Gln Arg Glu Pro Ile Cys Cys Phe Asp Ser Ile Pro Cys  
                   20                  25                  30

gct gat gga cac gtg tca cgg aaa cca ggt gaa agg gag tgt gaa caa 144  
 Ala Asp Gly His Val Ser Arg Lys Pro Gly Glu Arg Glu Cys Glu Gln  
                   35                  40                  45

tgt ggt gaa gac tat tgg tca aat gca caa aag agc gag tgt gtg ctg 192  
 Cys Gly Glu Asp Tyr Trp Ser Asn Ala Gln Lys Ser Glu Cys Val Leu  
                   50                  55                  60

aaa gag gtg gaa tac ctt gct tat gat gag gcc ctg gga ttc aca ctt 240  
 Lys Glu Val Glu Tyr Leu Ala Tyr Asp Glu Ala Leu Gly Phe Thr Leu  
                   65                  70                  75                  80

gtc att ctt tct gtc ttt ggg gca ttt gtg gtc ttg gca gtc aca gct 288  
 Val Ile Leu Ser Val Phe Gly Ala Phe Val Val Leu Ala Val Thr Ala  
                   85                  90                  95

gtg tat gtg ata cac agg cac act ccc ctg gtg aac gcc agt gac tgg 336  
 Val Tyr Val Ile His Arg His Thr Pro Leu Val Asn Ala Ser Asp Trp  
                   100                  105                  110

cag ctg ggc ttt ctc att cag gtt tct ctg atc atc atg ctg ctg tct 384  
 Gln Leu Gly Phe Leu Ile Gln Val Ser Leu Ile Ile Met Leu Leu Ser  
                   115                  120                  125

tcc atg ctt ttc att gac aag cca cac aac tgg tcc tgc atg gct ggc 432  
 Ser Met Leu Phe Ile Asp Lys Pro His Asn Trp Ser Cys Met Ala Gly  
                   130                  135                  140

cag gtc act ctg gca ctg ggc ttt tct ctt tgc ctg tct tgc ctt ctt 480  
 Gln Val Thr Leu Ala Leu Gly Phe Ser Leu Cys Leu Ser Cys Leu Leu  
                   145                  150                  155                  160

gga aag act agt tca ctg ttt tta gcc tac aga att tcc aaa tcc aaa 528  
 Gly Lys Thr Ser Ser Leu Phe Leu Ala Tyr Arg Ile Ser Lys Ser Lys  
                   165                  170                  175

act caa ctt aca tcc atg cac ccc ctt tat cgg aaa atc att gtg cta 576

1000336  
 999999  
 1000336  
 999999

Thr Gln Leu Thr Ser Met His Pro Leu Tyr Arg Lys Ile Ile Val Leu	
180 185 190	
atc tct gtt cta gcg gag att ggc ata tgt aca gcc tac ttg ata ttg	624
Ile Ser Val Leu Ala Glu Ile Gly Ile Cys Thr Ala Tyr Leu Ile Leu	
195 200 205	
gaa cct ccc atg gta tac aag aac atg gaa tct caa aat aca aag atc	672
Glu Pro Pro Met Val Tyr Lys Asn Met Glu Ser Gln Asn Thr Lys Ile	
210 215 220	
att ctg gga tgc aat gaa att tcc ata gag ttt ttg tac tcg atg ttt	720
Ile Leu Gly Cys Asn Glu Ile Ser Ile Glu Phe Leu Tyr Ser Met Phe	
225 230 235 240	
gga att gat gcc ttc tta gcc ttg cta tgc ttt ctt aca act ttt gtg	768
Gly Ile Asp Ala Phe Leu Ala Leu Leu Cys Phe Leu Thr Thr Phe Val	
245 250 255	
gct cgc cag tta cca gat aat tac tat gaa gga aaa tgc atc acc ttt	816
Ala Arg Gln Leu Pro Asp Asn Tyr Tyr Glu Gly Lys Cys Ile Thr Phe	
260 265 270	
ggg atg ctt gtc ttt ttc atc att tgg atg tct ttt gtc cct gtt tat	864
Gly Met Leu Val Phe Phe Ile Ile Trp Met Ser Phe Val Pro Val Tyr	
275 280 285	
ttg agc acc aaa ggc aag ttc aaa atg gct gtg gaa ata ttt gca atc	912
Leu Ser Thr Lys Gly Lys Phe Lys Met Ala Val Glu Ile Phe Ala Ile	
290 295 300	
ttg gca tcc agc cat ggc ttg ttg ggt tgt ata ttt gct cct aag tgc	960
Leu Ala Ser Ser His Gly Leu Leu Gly Cys Ile Phe Ala Pro Lys Cys	
305 310 315 320	
ctc att att ttg ctg agg cca gag agg aac acc agt gaa att gtt tgt	1008
Leu Ile Ile Leu Leu Arg Pro Glu Arg Asn Thr Ser Glu Ile Val Cys	
325 330 335	
gga aga gtc tcc acc aca gat aat tgc atc caa ctg acc tca gct ttt	1056
Gly Arg Val Ser Thr Thr Asp Asn Cys Ile Gln Leu Thr Ser Ala Phe	
340 345 350	

gtg agc agt gag ctt aac aat acc aca gtg tca act gtt ctg gat gac 1104  
 Val Ser Ser Glu Leu Asn Asn Thr Thr Val Ser Thr Val Leu Asp Asp  
           355                          360                          365

aga gtt ttg att tac atg tgt cct ttg aag ctg caa 1140  
 Arg Val Leu Ile Tyr Met Cys Pro Leu Lys Leu Gln  
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<210> 5

<211> 380

<212> PRT

<213> Homo sapiens

<400> 5

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			20					25					30		
Ala	Asp	Gly	His	Val	Ser	Arg	Lys	Pro	Gly	Glu	Arg	Glu	Cys	Glu	Gln
		35					40					45			
Cys	Gly	Glu	Asp	Tyr	Trp	Ser	Asn	Ala	Gln	Lys	Ser	Glu	Cys	Val	Leu
	50					55					60				
Lys	Glu	Val	Glu	Tyr	Leu	Ala	Tyr	Asp	Glu	Ala	Leu	Gly	Phe	Thr	Leu
65					70					75					80
Val	Ile	Leu	Ser	Val	Phe	Gly	Ala	Phe	Val	Val	Leu	Ala	Val	Thr	Ala
			85						90					95	
Val	Tyr	Val	Ile	His	Arg	His	Thr	Pro	Leu	Val	Asn	Ala	Ser	Asp	Trp
			100					105					110		
Gln	Leu	Gly	Phe	Leu	Ile	Gln	Val	Ser	Leu	Ile	Ile	Met	Leu	Leu	Ser
		115					120					125			
Ser	Met	Leu	Phe	Ile	Asp	Lys	Pro	His	Asn	Trp	Ser	Cys	Met	Ala	Gly
	130					135					140				
Gln	Val	Thr	Leu	Ala	Leu	Gly	Phe	Ser	Leu	Cys	Leu	Ser	Cys	Leu	Leu
145					150					155					160
Gly	Lys	Thr	Ser	Ser	Leu	Phe	Leu	Ala	Tyr	Arg	Ile	Ser	Lys	Ser	Lys
				165					170					175	
Thr	Gln	Leu	Thr	Ser	Met	His	Pro	Leu	Tyr	Arg	Lys	Ile	Ile	Val	Leu
		180						185					190		
Ile	Ser	Val	Leu	Ala	Glu	Ile	Gly	Ile	Cys	Thr	Ala	Tyr	Leu	Ile	Leu
		195					200					205			
Glu	Pro	Pro	Met	Val	Tyr	Lys	Asn	Met	Glu	Ser	Gln	Asn	Thr	Lys	Ile
	210						215					220			

Ile Leu Gly Cys Asn Glu Ile Ser Ile Glu Phe Leu Tyr Ser Met Phe  
 225 230 235 240  
 Gly Ile Asp Ala Phe Leu Ala Leu Leu Cys Phe Leu Thr Thr Phe Val  
 245 250 255  
 Ala Arg Gln Leu Pro Asp Asn Tyr Tyr Glu Gly Lys Cys Ile Thr Phe  
 260 265 270  
 Gly Met Leu Val Phe Phe Ile Ile Trp Met Ser Phe Val Pro Val Tyr  
 275 280 285  
 Leu Ser Thr Lys Gly Lys Phe Lys Met Ala Val Glu Ile Phe Ala Ile  
 290 295 300  
 Leu Ala Ser Ser His Gly Leu Leu Gly Cys Ile Phe Ala Pro Lys Cys  
 305 310 315 320  
 Leu Ile Ile Leu Leu Arg Pro Glu Arg Asn Thr Ser Glu Ile Val Cys  
 325 330 335  
 Gly Arg Val Ser Thr Thr Asp Asn Cys Ile Gln Leu Thr Ser Ala Phe  
 340 345 350  
 Val Ser Ser Glu Leu Asn Asn Thr Thr Val Ser Thr Val Leu Asp Asp  
 355 360 365  
 Arg Val Leu Ile Tyr Met Cys Pro Leu Lys Leu Gln  
 370 375 380

<210> 6

<211> 1140

<212> DNA

<213> Artificial Sequence

<220>

<223> This degenerate nucleotide sequence encodes the amino acid sequence of SEQ ID NO:5.

<221> misc\_feature

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<223> n = A,T,C or G

<221> misc\_feature

<222> 285, 288, 291, 297, 306, 312, 315, 318, 321, 327, 330, 342, 345, 351, 360, 363, 366, 378, 381, 384, 387, 393, 408, 420, 429, 432, 438, 441, 444, 447, 450, 453, 459, 462, 468, 471, 477, 480, 483, 489, 492, 495, 498, 504, 507, 513, 519

<223> n = A,T,C or G



<221> misc\_feature

<222> 525, 531, 537, 540, 543, 552, 555, 561, 573, 576, 582, 585,  
588, 591, 600, 609, 612, 618, 624, 630, 633, 639, 657, 666,  
678, 681, 696, 708, 714, 723, 732, 738, 741, 744, 747, 756,  
759, 762, 768, 771, 774, 780, 783, 801, 813, 819, 825

<223> n = A,T,C or G

<221> misc\_feature

<222> 828, 849, 855, 858, 861, 867, 870, 873, 879, 894, 897, 909,  
915, 918, 921, 924, 930, 933, 936, 939, 951, 954, 963, 972,  
975, 978, 981, 987, 993, 996, 1005, 1011, 1014, 1017, 1020,  
1023, 1026, 1044, 1047, 1050, 1053, 1059, 1062, 1065

<223> n = A,T,C or G

<221> misc\_feature

<222> 1071, 1080, 1083, 1086, 1089, 1092, 1095, 1098, 1107, 1110,  
1113, 1128, 1131, 1137

<223> n = A,T,C or G

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ccnggngarm gngartgyga rcartgyggn gargaytayt ggwsnaaygc ncaraarwsn 180  
gartgygtny tnaargargt ngartayytn gcntaygayg argcnytnng nttyacnytn 240  
gtcnathytnw sngtnttygg ngcnttygti gtnyngcng tnacngcngt ntaygtcnath 300  
caymgncaya cncnytngt naaygcwns gaytggcary tnggnttyyt nathcargtn 360  
wsnytnatha thatgytnyt nwswnsatg ytnttyathg ayaarccna yaaytggsn 420  
tgyatggcng gncargtnac nytngcnytn ggnttywsny tntggytnws ntgyytnytn 480  
ggnaaracnw snwsnytnnt yytngcntay mgnathwsna arwsnaarac ncarytnacn 540  
wsnatgcayc cnytnaymg naarathath gtnytnathw sngtnytngc ngarathgg 600  
athtgyacng cntayytnat hytngarccn ccnatggtn ayaaraayat ggarwsncar 660  
aayacnaara thathytnng ntgyaaygar athwsnathg arttyytna ywsnatgtty 720  
ggcnathgayg cnttyytngc nytnytngt tytytnacna cnttygtngc nmgnacarytn 780  
ccngayaayt aytaygargg naartgyath acnttyggna tgytngtntt ytyathath 840  
tggatgwsnt tytnccngt ntayytnwsn acnaarggna arttyaarat ggcngtnar 900  
athtgyacna thytngcnw nwsncaygg ytnytnngnt gyathtgygc nccnaartgy 960  
ytnathathy tnytnmgnc ngarmgnaay acnwsngara thgtntgygg nmngtnwsn 1020  
acnacngaya aytgyathca rytnacwns gcnttygtw snwsngaryt naayaayacn 1080  
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<210> 7

<211> 2781

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Chimeric receptor.

&lt;221&gt; CDS

&lt;222&gt; (1)...(2781)

&lt;400&gt; 7

atg ttt gag agg cgc aaa gag caa gac gag gga cca gga atc cat gaa	48
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1 5 10 15	
ttt ctt gca ttt tta tgg gct gaa ttg ggc tct gaa gcc aaa gaa gag	96
Phe Leu Ala Phe Leu Trp Ala Glu Leu Gly Ser Glu Ala Lys Glu Glu	
20 25 30	
aaa gaa gaa gaa cgg acc tgc cgg ttg ctg ggc aag tgt gta gat gcc	144
Lys Glu Glu Glu Arg Thr Cys Arg Leu Leu Gly Lys Cys Val Asp Ala	
35 40 45	
gaa aac cat tcc ctt gtt att gga gga ctg ttt cct att gac tcc agg	192
Glu Asn His Ser Leu Val Ile Gly Gly Leu Phe Pro Ile Asp Ser Arg	
50 55 60	
acc atc cca gca aat gag tct att ttg gag cca gca tca gca aaa tgt	240
Thr Ile Pro Ala Asn Glu Ser Ile Leu Glu Pro Ala Ser Ala Lys Cys	
65 70 75 80	
gaa ggg ttt aac ttt cag aga ttc cgc tgg atg aaa gcc atg atc cac	288
Glu Gly Phe Asn Phe Gln Arg Phe Arg Trp Met Lys Ala Met Ile His	
85 90 95	
atg atc aag gag att aat aag agg aag gat att ttg ccc aac atc act	336
Met Ile Lys Glu Ile Asn Lys Arg Lys Asp Ile Leu Pro Asn Ile Thr	
100 105 110	
ctg ggc tat cag atc ttt gat acc tgt ttt acc atc tcc aaa tca gtg	384
Leu Gly Tyr Gln Ile Phe Asp Thr Cys Phe Thr Ile Ser Lys Ser Val	
115 120 125	
gaa gca gtc ttg gta ttt ctt aca ggg cag gaa gaa aac agg ccc aat	432

att gac ctc agc ctg ttt gtg ctg gaa atg att cat cat aac ata act 912  
Ile Asp Leu Ser Leu Phe Val Leu Glu Met Ile His His Asn Ile Thr  
290 295 300

gac Asp 305	agg Arg 305	aca Thr 305	tgg Trp 305	ata Ile 310	gcc Ala 310	acc Thr 310	gaa Glu 315	gcc Ala 315	tgg Trp 315	att Ile 315	acc Thr 315	tct Ser 320	gct Ala 320	ctc Leu 320	att Ile 320	960
gca Ala	aag Lys	cct Pro	gag Glu	tat Tyr 325	ttc Phe 325	ccc Pro	tat Tyr	ttt Phe	ggt Gly 330	gga Gly	act Thr	att Ile	gga Gly	ttt Phe 335	gca Ala	1008
aca Thr	cca Pro	aga Arg	agt Ser 340	gtt Val	ata Ile	cca Pro	gga Gly	cta Leu 345	aaa Lys	gaa Glu	ttt Phe	ctt Leu	tat Tyr 350	gat Asp	gta Val	1056
cac His	cct Pro	aac Asn 355	aag Lys	gat Asp	cca Pro	aat Asn	gat Asp 360	gtc Val	ttg Leu	acc Thr	att Ile	gaa Glu 365	ttc Phe	tgg Trp	caa Gln	1104
act Thr 370	gct Ala 370	ttt Phe	aac Asn	tgt Cys	acc Thr	tgg Trp 375	ccc Pro	aac Asn	agc Ser	agt Ser	gtt Val 380	cct Pro	tat Tyr	aac Asn	gtg Val	1152
gat Asp 385	cac His	aga Arg	gtg Val	aat Asn	atg Met 390	act Thr	ggg Gly	aaa Lys	gaa Glu	gac Asp 395	aga Arg	ctg Leu	tat Tyr	gac Asp	atg Met 400	1200
tct Ser	gat Asp	cag Gln	ctc Leu	tgc Cys 405	act Thr	gga Gly	gag Glu	gag Glu	aag Lys 410	ctg Leu	gaa Glu	gat Asp	ctg Leu	aaa Lys 415	aac Asn	1248
acc Thr	tat Tyr	ctg Leu	gat Asp	aca Thr	tca Ser	cag Gln	cta Leu	aga Arg	att Ile	aca Thr	aaa Lys	caa Gln	tgt Cys 430	aaa Lys	caa Gln	1296
gct Ala	gta Val	tat Tyr 435	gct Ala	ata Ile	gct Ala	cat His	ggc Gly 440	ctg Leu	gat Asp	cat His	ctc Leu	agc Ser 445	aga Arg	tgt Cys	caa Gln	1344
gaa Glu 450	ggg Gly	cag Gln	gga Gly	cca Pro	ttt Phe	ggc Gly 455	tca Ser	aat Asn	cag Gln	caa Gln	tgt Cys 460	gca Ala	tat Tyr	ata Ile	cct Pro	1392
acc Thr 465	ttt Phe	gat Asp	ttc Phe	tgg Trp	cag Gln	cta Leu	atg Met	tac Tyr	tat Tyr	atg Met	aaa Lys	gaa Glu	att Ile	aaa Lys	ttt Phe 480	1440

aaa Lys	tca Ser	cat His	gag Glu	gat Asp	aaa Lys	tgg Trp	gta Val	att Ile	ctg Leu	gat Asp	gat Asp	aat Asn	gga Gly	gat Asp	tgg Leu	1488	
				485					490					495			
aaa Lys	aat Asn	gga Gly	cac His	tat Tyr	gat Asp	gtc Val	cta Leu	aac Asn	tgg Trp	cac His	tta Leu	gat Asp	gat Asp	gag Glu	gga Gly	1536	
				500					505					510			
gaa Glu	att Ile	tcc Ser	ttt Phe	gtg Val	aca Thr	gtt Val	ggg Gly	aga Arg	ttt Phe	aac Asn	ttt Phe	aga Arg	tct Ser	aca Thr	aac Asn	1584	
				515					520					525			
ttt Phe	gag Glu	ctt Leu	gtt Val	att Ile	cca Pro	acg Thr	aat Asn	tct Ser	aca Thr	ata Ile	ttt Phe	tgg Trp	aac Asn	act Thr	gag Glu	1632	
				530					535					540			
tca Ser	tca Ser	agg Arg	ctt Leu	ccc Pro	cat His	tca Ser	gtg Val	tgt Cys	act Thr	gat Asp	gtg Val	tgt Cys	cct Pro	cct Pro	ggg Gly	1680	
				545					550					555			560
act Thr	gga Gly	agg Arg	gga Gly	ttc Phe	gtt Val	cag Gln	agg Arg	gaa Glu	cca Pro	ata Ile	tgc Cys	tgc Cys	ttt Phe	gac Asp	tcc Ser	1728	
				565					570					575			
atc Ile	cca Pro	tgt Cys	gct Ala	gat Asp	gga Gly	cac His	gtg Val	tca Ser	cgg Arg	aaa Lys	cca Pro	ggt Gly	gaa Glu	agg Arg	gag Glu	1776	
				580					585					590			
tgt Cys	gaa Glu	caa Gln	tgt Cys	ggt Gly	gaa Glu	gac Asp	tat Tyr	tgg Trp	tca Ser	aat Asn	gca Ala	caa Gln	aag Lys	agc Ser	gag Glu	1824	
				595					600					605			
tgt Cys	gtg Val	ctg Leu	aaa Lys	gag Glu	gtg Val	gaa Glu	tac Tyr	ctt Leu	gct Ala	tat Tyr	gat Asp	gag Glu	gcc Ala	ctg Leu	gga Gly	1872	
				610					615					620			
ttc Phe	aca Thr	ctt Leu	gtc Val	att Ile	ctt Leu	tct Ser	gtc Val	ttt Phe	ggg Gly	gca Ala	ttt Phe	gtg Val	gtc Val	ttg Leu	gca Ala	1920	
				625					630					635			640
gtc	aca	gct	gtg	tat	gtg	ata	cac	agg	cac	act	ccc	ctg	gtg	aac	gcc	1968	

Val Thr Ala Val Tyr Val Ile His Arg His Thr Pro Leu Val Asn Ala  
 645 650 655

agt gac tgg cag ctg ggc ttt ctc att cag gtt tct ctg atc atc atg 2016  
 Ser Asp Trp Gln Leu Gly Phe Leu Ile Gln Val Ser Leu Ile Ile Met  
 660 665 670

ctg ctg tcg tcc atg ctt ttc att gac aag cca cac aac tgg tcc tgc 2064  
 Leu Leu Ser Ser Met Leu Phe Ile Asp Lys Pro His Asn Trp Ser Cys  
 675 680 685

atg gct ggc cag gtc act ctg gca ctg ggc ttt tct ctt tgc ctg tct 2112  
 Met Ala Gly Gln Val Thr Leu Ala Leu Gly Phe Ser Leu Cys Leu Ser  
 690 695 700

tgc ctt ctt gga aag act agt tca ctg ttt tta gcc tac aga att tcc 2160  
 Cys Leu Leu Gly Lys Thr Ser Ser Leu Phe Leu Ala Tyr Arg Ile Ser  
 705 710 715 720

aaa tcc aaa act caa ctt aca tcc atg cac ccc ctt tat cgg aaa atc 2208  
 Lys Ser Lys Thr Gln Leu Thr Ser Met His Pro Leu Tyr Arg Lys Ile  
 725 730 735

att gtg cta atc tct gtt cta gcg gag att ggc ata tgt aca gcc tac 2256  
 Ile Val Leu Ile Ser Val Leu Ala Glu Ile Gly Ile Cys Thr Ala Tyr  
 740 745 750

ttg ata ttg gaa cct ccc atg gta tac aag aac atg gaa tct caa aat 2304  
 Leu Ile Leu Glu Pro Pro Met Val Tyr Lys Asn Met Glu Ser Gln Asn  
 755 760 765

aca aag atc att ctg gga tgc aat gaa att tcc ata gag ttt ttg tac 2352  
 Thr Lys Ile Ile Leu Gly Cys Asn Glu Ile Ser Ile Glu Phe Leu Tyr  
 770 775 780

tcg atg ttt gga att gat gcc ttc tta gcc ttg cta tgc ttt ctt aca 2400  
 Ser Met Phe Gly Ile Asp Ala Phe Leu Ala Leu Leu Cys Phe Leu Thr  
 785 790 795 800

act ttt gtg gct cgc cag tta cca gat aat tac tat gaa gga aaa tgc 2448  
 Thr Phe Val Ala Arg Gln Leu Pro Asp Asn Tyr Tyr Glu Gly Lys Cys  
 805 810 815

atc acc ttt ggg atg ctt gtc ttt ttc atc att tgg atg tct ttt gtc 2496  
 Ile Thr Phe Gly Met Leu Val Phe Phe Ile Ile Trp Met Ser Phe Val  
                   820                                  825                                  830

cct gtt tat ttg agc acc aaa ggc aag ttc aaa atg gct gtg gaa ata 2544  
 Pro Val Tyr Leu Ser Thr Lys Gly Lys Phe Lys Met Ala Val Glu Ile  
                   835                                  840                                  845

ttt gca atc ttg gca tcc agc cat ggc ttg ttg ggt tgt ata ttt gct 2592  
 Phe Ala Ile Leu Ala Ser Ser His Gly Leu Leu Gly Cys Ile Phe Ala  
                   850                                  855                                  860

cct aag tgc ctc att att ttg ctg agg cca gag agg aac acc agt gaa 2640  
 Pro Lys Cys Leu Ile Ile Leu Leu Arg Pro Glu Arg Asn Thr Ser Glu  
                   865                                  870                                  875                                  880

att gtt tgt gga aga gtc tcc acc aca gat aat tgc atc caa ctg acc 2688  
 Ile Val Cys Gly Arg Val Ser Thr Thr Asp Asn Cys Ile Gln Leu Thr  
                                   885                                  890                                  895

tca gct ttt gtg agc agt gag ctt aac aat acc aca gtg tca act gtt 2736  
 Ser Ala Phe Val Ser Ser Glu Leu Asn Asn Thr Thr Val Ser Thr Val  
                   900                                  905                                  910

ctg gat gac aga gtt ttg att tac atg tgt cct ttg aag ctg caa 2781  
 Leu Asp Asp Arg Val Leu Ile Tyr Met Cys Pro Leu Lys Leu Gln  
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<210> 8

<211> 927

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric receptor.

<400> 8

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Phe	Leu	Ala	Phe	Leu	Trp	Ala	Glu	Leu	Gly	Ser	Glu	Ala	Lys	Glu	Glu
			20					25					30		

Lys	Glu	Glu	Glu	Arg	Thr	Cys	Arg	Leu	Leu	Gly	Lys	Cys	Val	Asp	Ala	
		35					40					45				
Glu	Asn	His	Ser	Leu	Val	Ile	Gly	Gly	Leu	Phe	Pro	Ile	Asp	Ser	Arg	
	50					55					60					
Thr	Ile	Pro	Ala	Asn	Glu	Ser	Ile	Leu	Glu	Pro	Ala	Ser	Ala	Lys	Cys	
65					70					75					80	
Glu	Gly	Phe	Asn	Phe	Gln	Arg	Phe	Arg	Trp	Met	Lys	Ala	Met	Ile	His	
			85					90						95		
Met	Ile	Lys	Glu	Ile	Asn	Lys	Arg	Lys	Asp	Ile	Leu	Pro	Asn	Ile	Thr	
		100						105					110			
Leu	Gly	Tyr	Gln	Ile	Phe	Asp	Thr	Cys	Phe	Thr	Ile	Ser	Lys	Ser	Val	
	115						120					125				
Glu	Ala	Val	Leu	Val	Phe	Leu	Thr	Gly	Gln	Glu	Glu	Asn	Arg	Pro	Asn	
	130					135				140						
Phe	Arg	Asn	Ser	Thr	Gly	Ala	Phe	Pro	Ala	Gly	Ile	Val	Gly	Ala	Gly	
145					150					155					160	
Gly	Ser	Phe	Leu	Ser	Val	Pro	Ala	Ser	Arg	Ile	Leu	Gly	Leu	Tyr	Tyr	
			165						170					175		
Leu	Pro	Gln	Val	Gly	Tyr	Thr	Ser	Thr	Cys	Val	Ile	Leu	Ser	Asp	Lys	
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Tyr	Gln	Phe	Pro	Ser	Tyr	Leu	Arg	Val	Ile	Ala	Ser	Asp	Lys	Ile	Gln	
	195						200					205				
Ser	Lys	Ala	Val	Val	Lys	Arg	Ile	Gln	His	Phe	Gly	Trp	Val	Trp	Val	
	210					215					220					
Gly	Ala	Ile	Ala	Ala	Asp	Asp	Asp	Tyr	Gly	Lys	Tyr	Gly	Val	Lys	Thr	
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Phe	Lys	Glu	Lys	Met	Glu	Ser	Ala	Asn	Leu	Cys	Val	Ala	Phe	Ser	Glu	
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Thr	Ile	Pro	Lys	Val	Tyr	Ser	Asn	Glu	Lys	Met	Gln	Lys	Ala	Val	Lys	
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Ala	Val	Lys	Thr	Ser	Thr	Ala	Lys	Val	Ile	Val	Leu	Tyr	Thr	Ser	Asp	
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Ile	Asp	Leu	Ser	Leu	Phe	Val	Leu	Glu	Met	Ile	His	His	Asn	Ile	Thr	
	290					295					300					
Asp	Arg	Thr	Trp	Ile	Ala	Thr	Glu	Ala	Trp	Ile	Thr	Ser	Ala	Leu	Ile	
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Ala	Lys	Pro	Glu	Tyr	Phe	Pro	Tyr	Phe	Gly	Gly	Thr	Ile	Gly	Phe	Ala	
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Thr	Pro	Arg	Ser	Val	Ile	Pro	Gly	Leu	Lys	Glu	Phe	Leu	Tyr	Asp	Val	
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His	Pro	Asn	Lys	Asp	Pro	Asn	Asp	Val	Leu	Thr	Ile	Glu	Phe	Trp	Gln	
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Thr	Ala	Phe	Asn	Cys	Thr	Trp	Pro	Asn	Ser	Ser	Val	Pro	Tyr	Asn	Val
370						375					380				
Asp	His	Arg	Val	Asn	Met	Thr	Gly	Lys	Glu	Asp	Arg	Leu	Tyr	Asp	Met
385					390					395					400
Ser	Asp	Gln	Leu	Cys	Thr	Gly	Glu	Glu	Lys	Leu	Glu	Asp	Leu	Lys	Asn
				405					410					415	
Thr	Tyr	Leu	Asp	Thr	Ser	Gln	Leu	Arg	Ile	Thr	Lys	Gln	Cys	Lys	Gln
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Ala	Val	Tyr	Ala	Ile	Ala	His	Gly	Leu	Asp	His	Leu	Ser	Arg	Cys	Gln
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Glu	Gly	Gln	Gly	Pro	Phe	Gly	Ser	Asn	Gln	Gln	Cys	Ala	Tyr	Ile	Pro
	450					455					460				
Thr	Phe	Asp	Phe	Trp	Gln	Leu	Met	Tyr	Tyr	Met	Lys	Glu	Ile	Lys	Phe
465					470					475					480
Lys	Ser	His	Glu	Asp	Lys	Trp	Val	Ile	Leu	Asp	Asp	Asn	Gly	Asp	Leu
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	530					535					540				
Ser	Ser	Arg	Leu	Pro	His	Ser	Val	Cys	Thr	Asp	Val	Cys	Pro	Pro	Gly
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Thr	Gly	Arg	Gly	Phe	Val	Gln	Arg	Glu	Pro	Ile	Cys	Cys	Phe	Asp	Ser
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Cys	Glu	Gln	Cys	Gly	Glu	Asp	Tyr	Trp	Ser	Asn	Ala	Gln	Lys	Ser	Glu
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Cys	Val	Leu	Lys	Glu	Val	Glu	Tyr	Leu	Ala	Tyr	Asp	Glu	Ala	Leu	Gly
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Val	Thr	Ala	Val	Tyr	Val	Ile	His	Arg	His	Thr	Pro	Leu	Val	Asn	Ala
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Ser	Asp	Trp	Gln	Leu	Gly	Phe	Leu	Ile	Gln	Val	Ser	Leu	Ile	Ile	Met
			660					665					670		
Leu	Leu	Ser	Ser	Met	Leu	Phe	Ile	Asp	Lys	Pro	His	Asn	Trp	Ser	Cys
		675					680					685			
Met	Ala	Gly	Gln	Val	Thr	Leu	Ala	Leu	Gly	Phe	Ser	Leu	Cys	Leu	Ser
	690					695					700				

Cys Leu Leu Gly Lys Thr Ser Ser Leu Phe Leu Ala Tyr Arg Ile Ser  
 705 710 715 720  
 Lys Ser Lys Thr Gln Leu Thr Ser Met His Pro Leu Tyr Arg Lys Ile  
 725 730 735  
 Ile Val Leu Ile Ser Val Leu Ala Glu Ile Gly Ile Cys Thr Ala Tyr  
 740 745 750  
 Leu Ile Leu Glu Pro Pro Met Val Tyr Lys Asn Met Glu Ser Gln Asn  
 755 760 765  
 Thr Lys Ile Ile Leu Gly Cys Asn Glu Ile Ser Ile Glu Phe Leu Tyr  
 770 775 780  
 Ser Met Phe Gly Ile Asp Ala Phe Leu Ala Leu Leu Cys Phe Leu Thr  
 785 790 795 800  
 Thr Phe Val Ala Arg Gln Leu Pro Asp Asn Tyr Tyr Glu Gly Lys Cys  
 805 810 815  
 Ile Thr Phe Gly Met Leu Val Phe Phe Ile Ile Trp Met Ser Phe Val  
 820 825 830  
 Pro Val Tyr Leu Ser Thr Lys Gly Lys Phe Lys Met Ala Val Glu Ile  
 835 840 845  
 Phe Ala Ile Leu Ala Ser Ser His Gly Leu Leu Gly Cys Ile Phe Ala  
 850 855 860  
 Pro Lys Cys Leu Ile Ile Leu Leu Arg Pro Glu Arg Asn Thr Ser Glu  
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 Ile Val Cys Gly Arg Val Ser Thr Thr Asp Asn Cys Ile Gln Leu Thr  
 885 890 895  
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<210> 9

<211> 2781

<212> DNA

<213> Artificial Sequence

<220>

<223> This degenerate nucleotide sequence encodes the amino acid sequence of SEQ ID:8.

<221> misc\_feature

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<223> n = A,T,C or G

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ytntynggna	artgygtnga	ygcngaraay	caywsnytn	tnathggngg	nytnntyccn	180
athgaywsnm	gnacnathcc	ngcnaaygar	wsnathytn	arccngcnws	ngcnaartgy	240
garggnttya	ayttycarmg	nttymgntgg	atgaargcna	tgathcayat	gathaargar	300
athaayaarm	gnaargayat	hytnccnaay	athacnytn	gntaycarat	httygayacn	360
tgyttyacna	thwsnaarws	ngtngargcn	gtntyngtnt	tyytnacngg	ncargargar	420
aaymgncna	ayttymgnaa	ywsnacnggn	gcnttyccng	cnggnathgt	ngngcnggn	480
ggwnsntty	tnwsngtncc	ngcnwsnmgn	athytnngny	tnaytayyt	nccncargtn	540
ggntayacnw	snacntgygt	nathytnwsn	gayaartayc	arttyccnws	ntayytnmgn	600
gtnathgcnw	sngayaarat	hcarwsnaar	gcngtngtna	armgnathca	rcayttyggn	660
tggtntggt	tngngcnat	hgcnngcnay	gaygaytayg	gnaartaygg	ngtnaaracn	720
ttyaargara	aratggarws	ngcnaaytn	tgygtngcnt	tywsngarac	nathccnaar	780
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gtnathgtnt	tnayacnws	ngayathgay	ytnwsnytn	tygtntynga	ratgathcay	900
cayaayatha	cngaymgna	ntggathgcn	acngargcnt	ggathacnws	ngcnytnath	960
gcnaarccng	artayttycc	ntayttyggn	ggnacnathg	gnttygcnac	nccnmgnwsn	1020
gtnathccng	gnytnaarga	rttyytnay	gaygtncayc	cnaayaarga	yccnaaygay	1080
gtntytnacna	thgarttytg	gcaraacngcn	ttyaaytgya	cntggccnaa	ywsnwsngtn	1140
ccntayaayg	tngaycaymg	ngtnaayatg	acnggnaarg	argaymgnyt	ntaygayatg	1200
wsngaycary	tnthyacngg	ngargaraar	ytngargayy	tnaaraayac	ntayytngay	1260
acnwsncary	tnmgnaathac	naarcartgy	aarcargcng	tnaygcnat	hgcnayggn	1320
ytngaycayy	tnwsnmgtg	ycargarggn	carggncnt	tyggwnsnaa	ycarcartgy	1380
gcntayathc	cnacnttyga	ytytggtcar	ytnatgtayt	ayatgaarga	rathaartty	1440
aarwsncayg	argayaartg	ggtnathytn	gaygayaayg	gngayytnaa	raayggncay	1500
taygaygtnt	tnaaytgga	yytngaygay	garggngara	thwsnttygt	nacngtnggn	1560
mgnttyaayt	tymgnwsnac	naaytygar	ytngtnathc	cnacnaayws	nacnathtty	1620
tggaayacng	arwsnwsnmg	nytnccncay	wsngtntgya	cngaygtntg	yccncenggn	1680
acnggnmgng	gnttygtnc	rmngnarccn	athgtgyt	tygaywsnat	hccntgygcn	1740
gayggncayg	tnwsnmgnaa	rccnggngar	mgngartgyg	arcartgygg	ngargaytay	1800
tggsnaayg	cncaraarws	ngartgygt	ytnaargarg	tngartayyt	ngcntaygay	1860
gargcnytn	gnttyacnyt	ngtnathytn	wsngtnttyg	gngcnttygt	ngtnytnngcn	1920
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garttyytn	aywsnatgtt	yggcnathgay	gcnttyytn	cnytnytn	yttyytnacn	2400
acnttygtng	cnmgncaryt	nccngayaay	taytaygarg	gnaartgyat	hacnttyggn	2460
atgytngtnt	tytyyathat	htggatgwsn	tygtncng	tnayytnws	nacnaarggn	2520

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tgyathhtyg cncnaartg yytnathath ytnytmgnc cngarmgnaa yacnwsngar 2640  
athgtntgyg gnmngtnws nacnacngay aaytgyathc arytnacnws ngcnttygtn 2700  
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<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide linker.

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